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SUMMARIES

Description	Sequence 15, Appl	Seguence 19, Appl	Sequence 15, Appl	Sequence 19, Appl	Sequence 15, Appl	Sequence 19, Appl	-	_	Sequence 1, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 11, Appl	
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Sequence 19, Application US/10682420

Publication No. US20040062775A1

GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: Le CANN, Pierre

APPLICANT: Le CANN, Pierre

APPLICANT: ARMAULD, Claire

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    GTTGTTTGGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGGGTAAAGTACCG
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PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SEQ ID NO 15
LENGTH: 1767
                                                                                                                                                       TYPE: DNA ORGANISM: Type B PWD circovirus
2003-04-09
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(1237)..(1359)
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(1363)..(1476)
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(808)..(861)
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NAME/KEY: CDS
LOCATION: (115)..(243)
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(451)..(471)
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(514)..(516)
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(733)...(753)
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(757)..(759)
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LOCATION: (247)..(267)
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(364)..(417)
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(475)..(510)
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(520)..(729)
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CURRENT FILING DATE:
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APPLICANT: BLANCHARD, Phillipe
APPLICANT: BLANCHARD, Phillipe
APPLICANT: BLANCHARD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: MARE, Dominique
APPLICANT: MADEC, Francois
TITLE OF INVENTION: DISEASE (FWD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/409,613
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US-10-409-613-15
Sequence 15, Application US/10409613
Publication No. US20040076635A1
GENERAL INFORMATION:
APPLICANT: ALBINA, Emanuel
APPLICANT: BLANCHARD, Phillipe
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: TRUONG, CATHERINE
APPLICANT: TRUONG, CATHERINE
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APPLICANT: ALBINA, Emanuel
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: DISEASE (PWD)
FILE REFERENCE: 065691/0176
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                            TTTTATTATTCATTAAGGGTTAAGTGGGGGGTCTTTAAAATTAAAATTCTCTGAAATTGTAA
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Publication No. US2040076635A1
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
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Matches 1767; Conservative
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Pred. No. 0;
); Mismatches
CURRENT APPLICATION NUMBER: US/10/409,613
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/09/514,245B
PRIOR PILING DATE: 2000-02-28
PRIOR PILING DATE: 2000-02-28
PRIOR PILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
LENGTH: 1767
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Matches 1767; Conservative
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; ORGANISM: Type ]
US-10-409-613-19
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Sequence 15, Application US/10442180; Publication No. US20040091502A1; GENERAL INFORMATION: APPLICANT: JESTIN, Andre APPLICANT: ALBINA, Emanuel RESULT 5 US-10-442-180-15

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Best Local Similarity 100.
Matches 1767; Conservative
                      FEATURE:
NAME/KEY: CDS
LOCATION: (1237) .. (1359)
FEATURE:
NAME/KEY: CDS
LOCATION: (1363) .. (1476)
FEATURE:
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LOCATION: (1480)..(1737)
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; NAME/KEY: CDS
; LOCATION: (1741)..(1767)
US-10-442-180-15
LÖCATION: (1177)..(1233)
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                  APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: HUTET, Evelyne
APPLICANT: ARMAULD, Claire
APPLICANT: RANAULD, Claire
APPLICANT: RANAULD, Claire
APPLICANT: MAHE, Dominique
APPLICANT: MADEC, Francois
TITLE OF INVENTION: DISEASE (PWD)
FILLE OF INVENTION: DISEASE (PWD)
FILLE OF INVENTION: DISEASE (PWD)
FILLE OF INVENTION: DATE: 2003-05-21
FILLE PREPERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
FRIOR APPLICATION NUMBER: US/09/514,245
FRIOR PLING DATE: 2000-02-28
FRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
SOFTWARE: NAMED AND ADDRESS OF AD
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LOCATION: (1)..(111)
FEATURE:
NAME/KEY: CDS
LOCATION: (115)..(243)
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LOCATION: (247)..(267)
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LOCATION: (271)..(360)
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Le CANN, Pierre BLANCHARD, Phillipe HUTET, Evelyne ARNAULD, Claire TRUONG, Catherine

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Sequence 19, Application US/10442180 Publication No. US20040091502A1 GENERAL INFORMATION: APPLICANT: JESTIN, Andre

RESULT 6 US-10-442-180-19/c

1168 1408 1228 1708 1528 480 540 009 9 360 APPLICANT: ANOUNCE, CALLELANDE
APPLICANT: MAHE, Dominique
APPLICANT: CARICUET, Roland
APPLICANT: CARICUET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
FILE REPERBNCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT PILING DATE: 2003-05-21
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0 TICTGAAGAAGCAGACTITIAATAAAGTGAAGTGGTATTTGGGTGCCCGCTGCCACATCG 300 240 120 TCAGAAATTTCCGCGGGCTGGCTGAACTTTTGAAAGTGAGCGGGAAAATGCAGAAGCGTG ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG ATTGGAAGACTAATGTACACGTCATTGTGGGGCCACCTGGGTGTGGTAAAAGCAAATGGG CIGCIAAITITIGCAGACCCCGGAAACCACAIACTGGAAACCACTAGAAACAAGTGGTGGG Trorrecceácica de contra de AGAAAGCGAAAGGAACAGATCAGCAGAATAAAGAATACTGCAGTAAAGAAGGCAACTTAC TGATGGAGTGTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA GTACCTTGTTGGAGGGGGGAGTCTGGTGACCGTTGCAGAGCAGCACCCTGTAACGTTTG AGAAGAATGGAAGAGGGGACCCCCATAAAAAGGTGGGTGTTCACTCTGAATAATC CTTCCGAAGACGAGCGCAAGAAATACGGGATCTTCCAATATCCCTATTTGATTTTTA 1 ACCAGGGGCACTTCGGCAGCAGCACCTCGGCAGCACCTCAGCAGCACATGCCCAGCA DB 16; Length 1767; Indels ö ; Score 1767; I ; Pred. No. 0; 0; Mismatches ; ORGANISM: Type B PWD circovirus US-10-442-180-19 Query Match 100.0%; Best Local Similarity 100.0%; Matches 1767; Conservative 0; SEO ID NO 19 LENGTH: 1767 1347 1227 1167 541 481 1287 601 1647 181 301 421 121 1587 241 TYPE: DNA ò g ð

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Qy 1741 AAACGAAAGAAGTGCGCTGTAAGTATT 1767 Db 27 AAACGAAAGAAGTGCGCTGTAAGTATT 1	RESULT 7 US-09-935-428A-1 i Sequence 1, Application US/09935428A i Patent No. US2020106639A1 i Patent No. US2020106639A1 i APPLICANT: WANG, LI APPLICANT: WALLSON, PHILIP ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING SYNDROME VIRUS FROM ITILE OF INVENTION: POSTWEAMING MULTISYSTEM WASTING NUMBER: 09/209,961 PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-10 PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-11 PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-16 NUMBER OF SEQ ID NOS: 24 SOFTWARE: PATENT NOW SERVED AND AND AND AND AND AND AND AND AND AN					Query Match 92.2%; Score 1629.6; DB 9; Length 1768; Best Local Similarity 95.5%; Pred. No. 0; Matches 1688; Conservative 0; Mismatches 79; Indels 1; Gaps 1;	OY 1 ACCAGGGACTTCGGCAGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCA 60	OY 61 AGAAGAATGGAAGAGCCCCACACCCCATAAAAGGTGGGTG	Oy 121 CTTCCGAAGACGCAAGAAAATACGGGATCTTCCAATATCCCTATTTGATTTTTA 180 121 CTTCCGAAGACGCCAAGAAATACGGGAGCTCCCCAATCTCCCTATTTGATTTTA 180		Qy 241 TIGIGAAGAAGCAGACTITTAATAAAGIGGAAGIGGTATITGGGIGCCCGCTGCCACATCG 300	Qy 301 AGADAGCGADAGGAACAGATCAGCAGDATADAGAATACTGCAGTADAGGAGGCAACTTAC 360	OY 361 TGATGGAGTCTGGAGCTCCTAGATCTCAGGGACAACGGAGTGACCTGTCTACTGCTGTGA 420 1	Oy 421 GTACCTTGTTGGAGGGGGGGTGTCTGGTGCTTGCTGGAGCAGCAGCACCTGTAACGTTTG 480	OY 481 TCAGAAATTTCGGGGCTGGCTGAACTTTTGAAAGTGAGGGGAAAATGCAGAAGGGG 540 	
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APPLICANT: MANG, LI
APPLICANT: BABIUK, LORNE A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: WILLSON, PHILLP
TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
TITLE OF INVENTION: PIGS
FILE REFERENCE: 9000-0040
CURRENT APPLICATION NUMBER: US/10/334,245
CURRENT APPLICATION NUMBER: LAS.
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/069,233
PRIOR PILING DATE: BARLIER FILING DATE: 1997-12-11
PRIOR PILING DATE: BARLIER FILING DATE: 1997-12-11
PRIOR PILING DATE: BARLIER FILING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PALENTIN VEY: 2.0
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                                                                                                                                                                         Sequence 1, Application US/10334245; Publication No. US20030170616A1; GENERAL INFORMATION:
                                           GATGGCTGCGGGGGGCGGTGTCTT
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Best Local Similarity 95.5%;
Matches 1688; Conservative
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US-10-334-245-11

Sequence 11, Application US/10334245

Publication No. US20030170616A1

GENERAL INFORMATION:

APPLICANT: WANG, LI

APPLICANT: WALLSON, POTTER, ANDREW A.

APPLICANT: WILLSON, PHILIP

TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM TITLE OF INVENTION: POSTWEANING MULTISYSTEM WASTING SYNDROME VIRUS FROM TITLE OF INVENTION: PIGS

FILE REFERENCE: 9000-0040

CURRENT APPLICATION NUMBER: US/10/334,245

CURRENT FILING DATE: 1099-12-10

PRIOR PILING DATE: EARLIER FILING DATE: 1997-12-11

PRIOR FILING DATE: EARLIER FILING DATE: 1997-12-11

PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1997-12-16

NUMBER OF SEQ ID NOS: 24

SEQ ID NO 11.
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92.1%; Score 1628; D:
Best Local Similarity 95.4%; Pred. No. 0;
Matches 1687; Conservative 0; Mismatches
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APPLICANT: WANG, LI
APPLICANT: BABIUK, LORNE A.
APPLICANT: BABIUK, LORNE A.
APPLICANT: POTTER, ANDREW A.
APPLICANT: WILLSON, PHILLP
TITLE OF INVENTION: POSTWERANING MULTISYSTEM WASTING SYNDROME VIRUS FROM
TITLE OF INVENTION: PIGS
TITLE OF INVENTION: PIGS
TITLE OF INVENTION: PIGS
CURRENT APPLICATION NUMBER: US/09/209,961
PRIOR PELLING DATE: EARLIER FILLING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: EARLIER FILLING DATE: 1999-12-11
PRIOR PILLING DATE: EARLIER FILLING DATE: 1997-12-11
PRIOR PILLING DATE: EARLIER FILLING DATE: 1997-12-11
PRIOR PILLING DATE: EARLIER FILLING DATE: 1997-12-11
PRIOR PILLING DATE: EARLIER FILLING DATE: 1997-12-16
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PARENTER FILLING DATE: 1997-12-16
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APPLICANT: ALLAN, Gordon
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APPLICANT: MEEHAN Brian
APPLICANT: GLAKK, Edward
APPLICANT: HARDING, John
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APPLICANT: HARDING, John
APPLICANT: CHARPEYE, Catherine E.
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APPLICANT: CHARPEYE, Catherine E.
APPLICANT: CHARPEYE, Francis McNeilly
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION NUMBER: US/09/884,514
CURRENT FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-01-22
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE PARCHILIN VET. 2.0
                                                                                                                                                                   1201 GTTGTTTGGTTGGAAGTAATCAATAGTGAAATCTAGGACAGGTTTGGGGGTAAAGTACCG
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                                                           ATACATGGTTACACGGATATTGTATTCCTGGTCGTATATACTGTTTTCGAACGCAGTGCC
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Best Local Similarity 99.6%;
Matches 1415; Conservative (
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- Web: www.genoscope.cns.fr

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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and malanogaster BAC library was prepared by Kazucoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                      BU059427 Fgr-C_02
BU061852 Fgr 1_A08
BU06060 Fgr-C_1_G
A1404106 GH23705.5
A1406114 GH26313.5
A1238565 GH14632.5
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/db_xref="taxon:7227"
/clone="BACR48P19"
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/note="end : TET3"
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(c) 1993 - 2004 Compugen Ltd
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Direct Submission

Direct Submission

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:

Bp 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

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Drosophila melanogaster genome survey sequence TET3 end of BAC:
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                                                                                                                1092 CACGGAFATTGTATTCCTGGTCGTATATACTGTTTTCGAACGCAGTGCCGAGGCCTACGT 1151
                                                                                                                                                                                                                                                                                                                                                                                 972 TITCCATATGAAATAAATTACTGAGTCTTTTTATCACTTCGTAATGGTTTTTATTTC
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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  Indels
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/mol_type="genomic DNA"
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/clone="BACR32D23"
  167;
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fly), genomic survey sequence. AL068607
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    139;
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      Conservative
      73;
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/note="end : TET3"
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CA297536 661 bp mRNA linear EST 26-SEP-2003
SCCCSDICO1F09.g SD1 Saccharum officinarum cDNA clone SCCCSDICO1F09
5', mRNA sequence.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae; Saccharum, Saccharum officinarum
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                                                                                             999 TITITIATCACTICGIAATGGTTTTTATTATTCATTAAGGGTTAAGTGGGGGGTCTTTAA 1058
                                                                                                                               1059 AATTAAATTCTCTGAATTGTACATGGTTACACGGATATTGTATTCCTGGTCGTATA 1118
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccenter.fcav.unesp.br
Plate: COl row: F column: 09
Seq primer: T7 Promoter Primer.
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/note="Organ: Developing seeds (large insert library);
Vector: pSport1; Site 1: Sa11; Site 2: Not1; An
unidirectional cDNA library generated from [Developing
                                                                                                                                                                                                                                                                                                                                                                                                  1179 TCAGCCACAGCTGGTTTCTTTTGTTTGGTTGGAAGTAATCAATAGTGAAATCTAGGA
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST Genet. MOI. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P. Contact: Arruda P. Contact Biologia Molecular e Engenharia Genetica Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Length 1101;
  2.7%; Score 47.8; DB 9; Length 1 ilarity 19.4%; Pred. No. 0.051; Conservative 135; Mismatches 151; Indels
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/lab_host="DH10B"
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Pred. No.

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Best Local Similarity 25.5%; Pr
Matches 103; Conservative 112;
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CA294389
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Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS0073W 922 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC #BACR14D09 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                            1582 GCGCGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTCCAGCGGTAACGGTGGCGGGG 1641
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                    polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                     insert library)]. cDNA was prepared from
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
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/mol_type="genomic DNA"
/db xref="taxon:7227"
                                                                                                                                                                                                      Score 46.6; DB 6; L
Pred. No. 0.097;
                                                                                                                                                                                                                                                                   0; Mismatches
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/clone lib="RPCI-98"
/note="end : TET3"
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1 Similarity 55.2%;
91; Conservative
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Length 922;

DB 9;

Score 46.6;

Query Match

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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unidirectional cDNA library generated from [Etiolated
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/note="Organ: Etiolated leaves from in vitro grown
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Clone digtribution: clone digtribution information can b
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.uneap.br
Plate: 012 row: B column: 06
Seg primer: T7 Promoter Primer.
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Contact: Arruda P
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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  188;
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/clone="SCSGLV1012B06"
/lab_host="DH10B"
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Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD
Slade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCSGLV1012B06.b LV1 Saccharum officinarum cDNA clone SCSGLV1012B06
leaves from in vitro grown sedlings]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between O.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at
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/db xref="taxon:4547"
/db xref="taxon:4547"
/db aref="sccglv1012B06"
/lab host="BH10B"
/clone lib="LV1"
/note="Organ: Eiolated leaves from in vitro grown
/note="Organ: Eiolated leaves from in vitro grown
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Emal: 519 3788 1089

Emal: partuda@unicamp.br
Clone distribution: clone distribution information can be f. clirough the Brazilian Clone Collection Center (BCCC) at thtp://www.bcccenter.feav.unesp.br
Plate: 012 row: B column: 06

Seq primer: SP6 Promoter primer.

Location/Qualifiers
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Vettore, A. L., da Silva, F.R., Kemper, B.L. and Arruda, P. The libraries that made SUCEST
The libraries that made SUCEST
Contact: Arruda P
Contact: Arruda P
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54.5%; Pred. No. 0.17;
ive 0; Mismatches 75; Indels
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/clone_lib="HRI"
//clone_lib="HRI"
//clone_lib="HRI"
//clone_logan: seedlings inoculated with Herbaspirilum
rubrisubalbicans; Vector: pSport1; Site_1: Sal1; Site_2:
Not1; An unidirectional cDNA library generated from
(seedlings inoculated with Herbaspirilum
rubrisubalbicans). cDNA was prepared from polyA+ mRNA
rubrisubalbicans). cDNA was prepared from polyA+ mRNA
using SuperScript plasmid System Kit (Invitrogen). The
using SuperScript plasmid System Kit (Invitrogen). The
club=strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
Spermatophyta; Magnoliophyta; Liliopsida; Saccharum officinarum
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SCSGHR1067F11.b HR1 Saccharum officinarum cDNA clone SCSGHR1067F11
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 067 row: F column: 11
Seg primer: SP6 Promoter primer.
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vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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/mol_type=t=x0n:4547"
/clone="SCSGHR1067F11"
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                                                                                                                                                                                                                            Score 45.6; DB
Pred. No. 0.19;
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Best Local Similarity 54.5%;
Matches 90; Conservative (
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/nol_type="mRNA"
/db_xref="texon:727"
/clone="GH27112"
/sex="male and female"
/dev_stage="adult"
/lab_host="DHS - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head; Vector: pOT2; Site_1: EcoR1; Site_2:
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BDGP/HHMI Drosophila EST Project
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 271 row: A column: 12
High quality sequence stop: 488.
1. ocation/Qualiflers
1. 551
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Query Match

2.6%; Score 45.6; DB 6; Length 667;

Best Local Similarity 54.5%; Pred. No. 0.19;

Matches 90; Conservative 0; Mismatches 75; Indels
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AIS14058.1 GI:4418120
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AG034053 1029 bp DNA linear GSS 01-NOV-2001
Pan troglodytes DNA, clone: PTB-009E13.F, genomic survey sequence.
AG034053
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CE373054 linear GSS 27-SEP-2003 tigr-gss-dog-17000362184725 Dog Library Canis familiaris genomic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Th: 301-838-0208
Email: ekirknes@tigr.org
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria, Carnivora; Fissipedia; Canidae; Canis.
1 (Dases 1 to 324)
Kirkness; E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          317 reactritrantecerranaearrecaearareaererrerrerrandaearerera
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/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"
                                                                                                                                                                                                                                                                                                                                                                                     and comparative analysis
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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1 Similarity 54.9%; Pred. No. 0.2;
89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  The dog genome: survey sequencing an Science 301 (5641), 1898-1903 (2003)
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/strain="Standard Poodle"
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                                                  genomic survey sequence.
CE373054
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                                                                                                             CE373054.1 GI:36596968
                                                                                                                                                                     Canis familiaris (dog)
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Best Local Similarity
Matches 89; Conserv
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COMMENT

rel: 302-631-2602

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Saccharum officinarum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1576 GAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTCTCCAGCGGTAACGGTG 1635
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SCEZHR1048D02.9 HR1 Saccharum officinarum cDNA clone SCEZHR1048D02
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Hi Line) immature anthers"
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Fax: 55 19 3788 1137  
Email: partuda@unicamp.br Clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br http://www.bcccenter.fcav.unesp.br Plate: 048 row: D column: 02  
Seq primer: T7 Promoter Primer.
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/note="Organ: seedlings inoculated with Herbaspirilum
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Contact: Arruda P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Indels
                                                                                                                                                                                                                                          /mol type="mRNA"
/db_xref="taxon:4565"
/clone="wialc.pk03.e22"
/tissue type="anthers"
/lab_host="DH108"
/lone_lib="wialc.pk108"
/clone_lib="wialc.pk108"
/note="Vector: pBluescript SK+; Si
XhoI; Wheat (Triticum aestivum, Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .603
/organism="Saccharum officinarum"
                                                                                                                                                                                                   /organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.5%; Score 45; DB 6;
Local Similarity 57.4%; Pred. No. 0.27;
Les 78; Conservative 0; Mismatches
        Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
Seq primer: M13.
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/db_xref="taxon:4547"
/clone="SCEZHR1048D02"
/lab_host="DH10B"
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EST.41621 CESTA444
                                                        2 (Bases I to 1021).

2 (Bases I to 1021).

Totoki,Y., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Submirro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

1-7-22 Submirro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

1-7-181-15-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the R&D process and may have higher chance of

clone tracking errors.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    978 TATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGTTTTTATTATTCATTAAG 1037
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E. I. DuPont de Nemours and Company
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
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2.6%; Score 45.2; DB 9; Length 1029;
Best Local Similarity 49.6%; Pred. No. 0.29;
Matches 116; Conservative 0; Mismatches 118; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-009E13.F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : pKS145
: SacI
: SacI
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                                       (bases 1 to 1029)
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R.Site 1
R.Site 2
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SOURCE
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JOURNAL
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TITLE

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Saccharum officinarum
Saccharum officinarum
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade, Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               1582 GCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTCTCCAGCGGTAACGGTGGCGGGG 1641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clome_lib="LV1"
hote="Corgan: Etiolated leaves from in vitro grown
sedlings; Vector: pSport1; Site 1: Sal1; Site 2: Not1; An
unidirectional cDNA library generated from [ETiolated
leaves from in vitro grown sedlings]. cDNA was prepared
from polyA+ mRNA using SuperScript Plasmid System Kit
(Invitrogen). The double-strand cDNAs were fractionated
                     Not; An unidirectional CDNA library generated from seedlings inoculated with Herbaspirilum rubrisubablicans! CDNA was prepared from polya+ mRNA using SuperScript Plasmid System Kit (Invirrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb ware directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccenter.fcav.unesp.br
Plate: 044 row: D column: 03
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
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                                                                                                                                                                                                                                                                                                                                            Score 45; DB 6; Length 603;
Pred. No. 0.28;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              217 Aceccecececicecececiaceciarececaacreceaeceaacresa 261
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Cantar Postal 610, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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/db_xref="taxon:4547"
/clone="SCSFLV1044D03"
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CA300454
CA300454.1 GI:36074598
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Best Local Similarity 54.5%;
Matches 90; Conservative
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CA300454
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/clone lib="FLI"
//oce="Organ: Inflorescence at begining of development
/note="Organ: Inflorescence at begining of development
(lcm-long); Vector: pSport1; Site=1: Salt; Site=2: NotI;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (lcm-long)].
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sixing between 0.8 and 1.5 KD were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCSGFL1079E04.g FL1 Saccharum officinarum cDNA clone SCSGFL1079E04
in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
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Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 079 row: E column: 04
Seq primer: T7 Promoter Primer.
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Contact: Arruda P
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                                                                                                                                                                                                                                                                                                                    2.5%; Score 45; DB 6; Length 622; 54.5%; Pred. No. 0.28; ive 0; Mismatches 75; Indels
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/db_xref="taxon:4547"
/clone="SCSGFL1079E04"
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CA198894
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/organism="Saccharum officinarum"
/organism="Saccharum officinarum"
/molt-type="mRNA"
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/clone="ScJFHRIC03A05"
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rubrisubalbicans; Vector: pSport1; Site 1: Sal1; Site_2:
Not1; An unidirectional cDNA library generated from
seedlings inoculated with Herbaspirilum
rubrisubalbicans] cDNA was prepared from poly4-mRNA
rubrisubalbicans] cDNA was prepared from poly4-mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs.were fractionated in a sepharose
CL-28 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
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Complex.

Systems 1 to 721)

Systems 2 to 721)

Systems 3 to 721)

Contact: No. 1 Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Contact: Biologia Molecular e Engenharia Genetica

Universidade Estedual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1137

Fax: 55 19 3788 1137

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.boccenter.fcav.unesp.br

Plate: CO3 row: A column: 05

Seq primer: T7 Promoter Primer.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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0; Mismatches 75; Indels
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                                          Score 45; DB 6;
Pred. No. 0.28;
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Jestin,A., Albina,E., Le Cann,P., Blanchard,P., Hutet,E.,
Jestin,A., Albina,C., Mahe,D., Cariolet,R. and Madec,F.
Circovirus sequences associated with piglet weight loss disease (PWD)
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ive 0; Mismatches
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ht loss disease (pwd) Indels 0; Gaps polarit + (5'-3')" Length 1767; virus.

1141 GAGGCCTACGTGGTCTACATTTCCAGCAGTTTGTAG	RESULT 5 AY321984 LOCUS DEFINITION PORTING CIRCOVIRUS 2 STRAIN Fd3, comply ACCESSION VERSION VERSION AY321984.1 GI:32478760 KEYWORDS SOURCE ORCANISM PORTING CIRCOVIRUS 2 VIRUSES: SOURCE ORCANISM PORTING CIRCOVIRUS 2 VIRUSES: SOURCE ORCANISM PORTING CIRCOVIRUS 2 VIRUSES: SOURCE I (bases 1 to 1767) AUTHORS GENERAL CHARACTERIZATION OF PORTING FORD AND AUTHORS FORD B. Molecular characterization of Porting non-affected pigs JOURNAL J. Gen. Virol. 85 (Pt 2), 293-304 (200 PUBMED) AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS AUTHORS SOURCE COCCESSION VIRUSES 1 to 1767) AUTHORS AUT
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                                                                                                                                                                                                          evidence=not_experimental product="ORF4"
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                                                                                 complement (386. .565)
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                                                                                                                                            gene="ORF4"
note="6.5 kDa"
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RITSLYFWKNATEQSTEEGGQFVTLSPPCPEFPYEINY"
/conplement(357. 671)
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Porcine circovirus 2
Viruses: BSDNA viruses; Circoviridae; Circovirus.

Viruses: BSDNA viruses; Circoviridae; Circovirus.

Viruses: Lo 1767)
Wellenberg, G.J., Pesch, S., Berndsen, F.W., Steverink, P.J.G.M.,
Hunneman, W., Van der Vorst, T.J.K., Peperkamp, N.H.M.T.,
Ohlinger, V.F., Schippers, R., Van Oirschot, J.T. and de Jong, M.F.
pigs showing signs of post-weaning multisystemic wasting syndrome in The Netherlands
Unpublished
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Direct Submission
Submitted (04-NOV-1999) Virology and Molecular Epidemiology,
BioScreen European Veterinary Disease Management Center GmbH, 11
Mendelstr., Muenster, NRW 48149, Germany
Location/Qualifiers
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Porcine circovirus type 2, complete genome. AF201897
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Oorganiam="Porcine circovirus 2"

mol type="genomic DNA"

/strain="24657 NL"
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complement(join(1731..1767,1.
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                                                 1741 AAACGAAAGAAGTGCGCTGTAAGTATT 1767
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51. .995
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GGAGTGGTAGGAGAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGTC 1320
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TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT
                            CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTTATCACTTCGTAATGGT
                                                                                                                                                                                          TITTATTATTCATTAAGGGTTAAGTGGGGGGGTTTTAAAATTAAAATTCTCTGAATTGTAC
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|gene="ORF7"
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/db xref="G1:32478765"
/translation="MTYPRRRYRRRHRPRSHLGQILRRRPWLVHPRHRYRWRRKNGI
FNTRLSRTFGYTVKRTTVRTPSWAVDNMRFNINDFLPPGGGSNPRSVPFEYYRIRKVK
VEFWPCSPITGGDRGVGSSAVILDDNFVTKATALTVDPYNNYSSRHTITQPFSYHSRY
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                                                                                             de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N., Eveno, E., Madec, F. and Jestin, A.
Molecular characterization of Porcine circovirus type 2 isolates from post-weaning multisystemic wasting syndrome-affected and non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
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de Boisseson,C., Beven,V., Bigarre,L., Thiery,R., Rose,N., Evenois., Madec,F. and Jestin,A.
Direct Submission
Submitted (11-70N-2003) Viral Genetics and Biosafety Unit Frod Safety Agency, BP 53, Ploufragan 22 440, France
Location/Qualifiers
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Viruses; ssDNA viruses; Circoviridae;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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Best Local Similarity 99.6%;
Matches 1760; Conservative
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RTSLYFWKNATEGGFREGGGPVTLSPPCPEFPYEINY"
complement (1033 . .1734)
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Viruses; sBNN viruses; Circoviridae; Circovirus.
1 (bases 1 to 1767)
de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
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GTCATTAATATTGAATCTCATGTCCACGCCCAGGAGGGCGTTCTGACTGTGGTTCG
                                                                                               GTCATTAATATTGAATCTCATCATGTCCACCGCCCCAGGAGGGCGTTCTGACTGTGGTTCG
                                                                                                                             CTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTCT
                                                                                                                                            CCAGCGGTAACGGTGGCGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAAG
                                                                                                                                                                                        CCAGCGGTAACGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGGGGATCTGGCCAAG
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Direct Submission
Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit Food Safety Agency, BP 53, Ploufragan 22 440, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Porcine circovirus
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Pred. No. 0;
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                                                                                                                                                                                                                                   /isolation_source="PDNS-affected pig lung, lymph node, and tonsil tissue"
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                                                                                Larrach, B.
Barrach, B.
Direct Submission
Submitted (14-MAR-2003) Veterinary Medical Research Institute,
Hungarian Academy of Sciences, Hungaria krt. 21, Budapest H-1143,
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                                    Characterisation of Hungarian porcine circovirus 2 genomes associated with PMMS and PDNS cases Acta Vet. Hung. 51 (4), 551-562 (2003)
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Dan,A., Molnar,T., Biksi,I., Glavits,R., Shaheim,M.A.
Harrach,B.
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/mol type="genomic DNA"
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51. .995
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/strain="375"
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Porcine circovirus type 2 strain 375 replicase (rep) and putative capsid protein (cap) genes, complete cds.

AY256460.1 GI:37595458
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                    GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGGCCCAGTTCGTCACCCTTTCCCCCC
                                     CATGCCCTGAATTTCCATATGAAATAAATTACTCAGTCTTTTTTATCACTTCGTAATGGT
                                                                                       CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT
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        /product="capsid"
/protein id="AAR83606.1"
/protein id="AAR83606.1"
/brotein id="AAR83606.1"
/trainslation="MYPPRREWFRRENEPRSHLGQILRRRPWLVHPRHRYRWRRKNGI
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VERPWCSPITQGDRGVGSSAVILDDNFVTKATALTYDPYVNYSSRHTITQPFSYYRRY
FTPRPVLDSTIDYFOPNKRNQLWLRLQTAGNVDHVGLGTAFENSIYDQEYNIRVTMY
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Porcine circovirus 2 Porcine circovirus 2 Viruses; ssDNA viruses; Circoviridae; Circovirus.

circular VRL 11-FEB-2004 genome.

complete DNA

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      1 (bases 1 to 1767)
de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.
Molecular characterization of Porcine circovirus type 2 isolates
from post-weaning multisystemic wasting syndrome-affected and
non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
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                                                                                                     Cases 1 to 1767)

de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N., Eveno, E., Madec, F. and Jestin, A.

Direct Submission
Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit Food Safety Agency, BP 53, Ploufragan 22 440, France
Location/Qualifiers
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; Pred. No. 0;
0; Mismatches
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ilarity 99.5%;
Conservative 0
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RITSLVFWKNATEQSTEEGGGFVTLSPPCFPFFFINY"
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                                                                                               CCAGCGGTAACGGTGGCGGGGGTGGACGAGCCAGGGGCGGCGGCGGAGGATCTGGCCAAG
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8 Kaixuan Road, Hangzhou,
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Zhou,J.Y., Chen,Q.X., Ye,J.X., Chen,W.J., Chen,J.G.,
Shang,S.B.
Shangsion
Submisted (26-NOV-2002) Institute of Preventive Veter
Medicine, Zhejiang University, 268 Kaixuan Road, Hang
110029, P.R.China
Location/Qualifiers
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Porcine circovirus 2
Viruses; seDNA viruses; Circoviridae; Circovirus.
1 (bases 1 to 1767)
Shou, J. Y., Chen, G.Y., Ye, J.X., Chen, W.J., Chen, J.G., Shang, S.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete genome of HZ0201 strain of PCV-2 isolated various clinical syndromes Unpublished
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780

780 840

720 720

and

Chen, W.J.

(bases 1 to 1767)

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organism="Porcine circovirus

/virion

/mol_type="genomic DNA" /strain="HZ0202" /specific host="pia" /db_xref="taxon: 85708" /country="China: Zhejiang" /note="genotype: PCV-2"

51. .995

and

Chen, W.J. sows with

Wang, J.Y., Chen, J.G.,

(bases 1

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Submitted (13-JAN-2003) Zhejiang University, Institute of Preventive Veterinary Medicine, 268 Kaixuan Road, Hangzhou Zhejiang 310029, P.R. China Location/Qualifiers
                                                                                       2 (bases 1 to 1767)
Zhou,J.Y., Chen,Q.X., Ye,J.X., Wang,J.Y., Chen,J.G.,
Zheng,X.J.
Direct Submission
                                                Complete genome of PCV-2 strain HZ0202 isolated from
Porcine circovirus 2
Viruses; ssDNA viruses; Circoviridae; Circovirus.
                      1 (bases 1 to 1/0/)
Zhou,J.Y., Chen,Q.X., Ye,J.X.,
Zheng,X.J.
                                                               various clinical syndrome
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    CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT
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FTPKPVLDSTIDYEOPNKRNQLWLRLQTAGNVDHVGLGTAFENSIYDQEYNTRYTWY
VQFREPNLKDPPLNP"
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larity 99.4%; Pred. No. 0;
Conservative 0; Mismatches
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/db_xref="GI:28932893"
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/gene="rep"
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1767 bp DNA circular VRL 12-MAR-2003 2 strain HZ0202, complete genome.

AY217743 Porcine circovirus type AY217743

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AY217743.1 GI:28932891 Porcine circovirus

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AY321988.1 GI:32478772
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de Boisseson,C., Beven,V., Bigarre,L., Thlery,R., Rose,N.,
Breno,E., Madec,F. and Jestin,A.
Direct Submission
Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit, French
Food Safety Agency, BP 53, Ploufragan 22 440, France
Location/Qualifiers
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Porcine circovirus 2

Viruses; seDNA viruses; Circoviridae; Circovirus.

1 (bases 1 to 1767)

de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N., Eveno, E., Madec, F. and Jestin, A.

Molecular characterization of Porcine circovirus type 2 isolates from post-weaning multisystemic wasting syndrome-affected and non-affected pigs
J. Gen. Virol. 85 (Pt 2), 293-304 (2004)
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GGAGTGGTAGGAGAAGGGCTGGGTTATGGTATGGCGGGAGGAGTAGTTTACATAGGGGGTC
                     GTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGCGTTCTGACTGTGGTTCG
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GWLPWNDDLLKLCDRFPLTVETKGGTVPFLAGILITSWQTPLEWYSSTAVPAVBALYR
RITSLVFWKNATEQSTEEGGQFVTLSPPCPEFPYEINY"
complement (1033 . .1734)
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VEPRKVLLDSTIDYFQPNNKRNQLWLRLGTAGNVDHVGLGTAFENSIYDQEYNIRVTMY
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                                                                   Virues, sebna viruses, Circoviridae, Circovirus.

1 (bases 1 to 1767)

6 Boisseson, C., Beva, V., Bigarre, L., Thiery, R., Rose, N.,
Eveno, E., Madec, F. and Jestin, A.

Molecular characterization of Porcine circovirus type 2 isc
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de Boisseson, C., Beven, V., Bigarre, L., Thiery, R., Rose, N., Berono, E., Madec, F. and Jestin, A.

Direct Submission
Submitted (11-JUN-2003) Viral Genetics and Biosafety Unit Food Safety Agency, BP 53, Ploufragan 22 440, France
1. .1767
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llarity 99.4%; Pred. No. 0;
Conservative 0; Mismatches 10;
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codon start=1
/product="replicase"
/proteci="replicase"
/db_xref="G1:32478779"
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ò	1441	TATTCTGTAGTATTCAAAGGGCACAGAGCGGGGGTTTGACCCCCCTCCTGGGGGAAGAAA 1500	
q	1441	TATTCTGTAGTATTCAAAGGGCACAGAGGGGGTTTGAGCCCCCTCCTGGGGGAAGAAA 1500	
λō	1501	GTCATTAATATTGAATCTCATCATCACCGCCCAGGAGGGGGGGTTCTGACTGTGGTTCG 1560	
ą	1501	GTCATTAATATTGAATCTCATCATGTCCACCGCCCAGGAGGGCGTTTTGACTGTGTTCG 1560	
ò	1561	CTTGACAGTATATCCGAAGGTGCGGGAGGGGGGGGTGTTGAAGATGCCATTTTTCCTTCT 1620	
q	1561	CITGATAGTATATCCGAAGGGGGGGGGGGGGTGTTTTTTTTT	
ζ	1621	CCAGGGGTAAACGGTGGGGGGGGGGGGGGGGGGGGGGGG	
අු	1621	CCAGCGGTAACGGTGGCGGGGGGGGGGCCAGGGGCGGCGGGGGGGTCTTTTTTTT	
Š	1681	ATGCTGCGGGGGGGGTGTCTTCGGTAACGCCTCCTTGGATACGTCATATCTGA 1740	
q	1681	AFGCTGCGGGGGGGGTGTTTTTTTTCCGGTAACGCCTTCGTTGGATACGTCATATCTGA 1740	
λō	1741	AAACGAAAGAAGTGCGCTGTAAGTATT 1767	
qq	1741	AAACGAAAGAAGTGCGCTGTAAGTATT 1767	
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/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-583-350-6	US-09-884-514-6	US-09-514-245-1	US-09-514-245-163	US-09-514-245-5	US-09-267-177-38	US-09-267-177-40	US-09-514-245-164	US-09-267-177-2	US-09-267-177-1	US-09-514-245-23	US-09-583-545-13	US-09-347-594-5	US-09-082-558-5	US-09-161-092-5	US-09-583-350-5	US-09-884-514-5	US-09-514-245-25
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APPLICANT: JESTINA, Emanuel
APPLICANT: JESTINA, Emanuel
APPLICANT: ALBINA, Emanuel
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APPLICANT: BLANCHARD, Phillipe
APPLICANT: HUTET, Evelyne
APPLICANT: HUTET, Evelyne
APPLICANT: TRUONG, Catherine
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: MADEC, Francois
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASF
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR PILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin version 3.0
ALIGNMENTS
                                                                                     ; Sequence 15, Application US/09514245; Patent No. 6703023; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Type B PWD circovirus
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                                                          APPLICANT: JESTIN, Andre
APPLICANT: JESTIN, Andre
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: BLANCHARD, Phillipe
APPLICANT: HATET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUGNG, Catherine
APPLICANT: TRUGNG, Catherine
APPLICANT: RANGULE, Roland
APPLICANT: RANGULE, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES AS
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES AS
FILE REFERENCE: 665691/0176
CURRENT APPLICATION NUMBER: US/09/514,245
CURRENT FILING DATE: 2000-02-28
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTIN VERSION 3.0
                            Sequence 19, Application US/09514245 Patent No. 6703023
                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Type B PWD circovirus
                                                   GENERAL INFORMATION:
APPLICANT: JESTIN,
APPLICANT: ALBINA,
                  -09-514-245-19/c
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                                                                                                                                                                                                                                                                  SOFTWARE:
SEQ ID NO 19
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	<i>ે</i> ઠ વે	601 CTGCTAATTTTGCAGACCGGAAACCACATACTGGAAACCACCTAGAAACAAGTGGTGGG 660
SULT 4 -09-583-350-7 Sequence 7, Application US/09583350 Patent No. 6517843	, & A	661 AIGGITACCAIGGIGAAGAGAGTIGITAITGATGACITITAAGGCIGGCTGCCCTGGG 720
L INFORMATION: CANT: Ellis, et al. CANT: Ellis, et al. CANT: ELLION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS OF INVENTION: WITH PORCINE CIRCOVIRUS-2	රු සි	721 ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAGGTGGAACTG 780
; FILE REFERENCE: 454313-2240.1 ; CURRENT APPLICATION VUNBER: US/09/583,350 ; PRIOR APPLICATION NUMBER: 60/151,564	& A	781 TACCTITITIGGCCCGCAGTAITCTGAITACCAGCAATCAGACCCGTTGGAATGGTACT 840
PRIOR FILING DATE: 1999-08-31 NUMBER OF SEQ 1D NOS: 8 SOFTWARE: PatentIn version 3.0 SOFT OF 17	& g	841 CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT 900
LENGTH: 1768. TYPB: DNA ORGANISM: Porcine circovirus	<u>ئ</u> ۾	901 GGAAGAATGCTACAGAATCCACGGAGGAAGGGGCCAGTTCGTCACCTTTCCCCCC 960
NAME/KEY: misc_feature LOCATION: (1). (1768) OTHER INFORMATION: nucleotide "k" can be either "g" or "t" and OTHER INFORMATION: nucleotide "y" can be either "c" or "t"	ò a	
Score 1636.8; DB 4; Length 1768; Pred. No. 0;	ζ di	1021 TITIATTATTCA-TTAAGGGTGTTAAGTGGGGGGTCTTTAAAATTAAATT
vative 2; Mismatches 74; Indels 1; Gaps CTTCGGCAGCGCAGCACCTCAGCAGCAACATGCCCAGCA	& 8	1080 CATACATGGTTACACGGATATTGTATTCCTGGTCGTATATACTGTTTTCGAACGCAGTGC 1139
ACCAGGGCACTTCGGCAGCGGCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCCAGCAAAAAAAA	& a	1140 CGAGGCCTACGTGCTACATTTCCAGCAGTTTGTAGTCTCAGCCACAGCTGGTTTCTTT 1199
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GGGGGGGGGGGCGGGATTCAACCTTAACCTTTC 1439 GGCACAGAGCGGGGTTTGACCCCCTCCTGGGGGAAGAA 1499 PATCATGTCCACCGCCCAGAGGGGTTCTGACTGTGGTTC 1559 GTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC 1619 TCAATAGTGAAATCTAGGACAGGTTTGGGGGTAAAGTACC 1259 TITCCAGCAGITIGIAGICCACCAGCTGGITICTIT STAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT TCCACGGAGGAAGGGGCCAGTTCGTCACCCTTTCCCCCCC

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qa -	<i>장</i> 名 	& A	<i>ò</i> a	ኤ a	<u>ራ</u> 8	& d	& 8 ————————————————————————————————————	<i>જે</i> વૈ	& a	& g	& 43 	0 n	S G	о <u>а</u>	<u> </u>	о р	α D
 crrc 162	Qy 1620 TCCAGCGGTAACGGTGGCGGGGTGGACGAGCGGGCGGCGGCGGGGGGAGATCTGGCCAA 1679 D	Qy 1680 GATGGCTGCGGGGGGGTGTCTTCTTCTTCGGTAACGCCTCCTTGGATACGTCATATCTG 1739 Db 1681 GATGGCTGCGGGGGGGGGTGTCTTCTTCTGGGGTAACGCCTCCTTGGATACGTCATAGGTG 1740	Qy 1740 AAAACGAAAGAAGTGCTGTAAGTATT 1767 Db 1741 AAAACGAAAGAAGTGCGCTGTAAGTATT 1768	RESULT 6 US-09-347-594-1	0.110	APPLICANT: MEHAN, Brian M. APPLICANT: ELLIS, John A. APPLICANT: RAKWKA, George S. APPLICANT: AUDONNET, Jean-Christophe F.		EARLIER APPLICATION NUMBER: 98 08777 SARLIER FILING DATE: 1998-07-06 NUMBER OF SEQ ID NOS: 5 SOFTWARE: PATENTI Ver. 2.1	O)	; Score 1412; DB 3; Length 1767; ; Pred. No. 0;	0, Mismatches 5, Indels 0, Gaps GGGCAGCACCTCAGCAGCACCAGCA	348 ACCAGCGCACTTCGGCAGCGCCAGCACCTCGGCAGCACCTCAGCAGCAACATGCCAGGA 61 AGAAGAATGGAAGAGGGACCCCAACCCCATAAAAGGTGGGTG	408 AGAAGAAGAAGAGGGGACCCCAACCCCATAAAAGGGGGGGG	181 TTGTTGGCGAGGGGAATGAGGAAGGACGAACTCCCTCCCCCCCC	Db 528 TIGTIGGCGAGGGGAAGGAAGGACGACCTCCAGGGGTTCGCTAAIT 587	301 AGARAGGARAGGARAGAGARGAGATAAAGAATACTGCAGTAAAGAAGGAACTTAC 	Oy 361 TGATGGAGTGTGGAGCTCCTAGATCTCAGGACAACGAGTGACCTGTCTACTGCTGTGTAGA 420 Db

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TITIATTATTCATTAAGGGTTTAAGTGGGGGGTCTTTAAAATTAAAATTCTCTGAATTGTAC 1080
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US-09-161-092-1
| Sequence 1, Application US/09161092
| Patent No. 6391314
| Patent No. 6391314
| GENERAL INFORMATION:
| APPLICANT: ALLAN, Gordon
| APPLICANT: HALBAN, Brian
| APPLICANT: HALBERY, Edward
| APPLICANT: HARBERY, Lori
| APPLICANT: HARBING, John
| APPLICANT: GHARPERYER, Catherine E. APPLICANT: GHARPERYER, Catherine E. TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
| TITLE OF INVENTION: REAGENTS
| FILE REFERENCE: ALLAN
| FILE REFERENCE: ALLAN
| CURRENT APPLICATION NUMBER: US/09/161,092
| CURRENT FILING DATE: 1998-09-25
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  APPLICANT: ALLAN, Gordon
APPLICANT: MEEHAN, Brian
APPLICANT: CLARK, Edward
APPLICANT: CLARK, Edward
APPLICANT: HANES, Deborah
APPLICANT: HANES, Lori
APPLICANT: HANDING, John
APPLICANT: HANDING, John
APPLICANT: CHARREYE, Catherine E.
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAG:
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAG:
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAG:
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND LIAN
CURRENT APPLICATION NUMBER: PR 9800873
EARLIER PILING DATE: 1998-01-22
EARLIER PILING DATE: 1998-01-22
EARLIER PILING DATE: 1998-03-20
SOFTWARE: PAPPLICATION NUMBER: FR 997/12382
EARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 0;
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Best Local Similarity 99.6%;
Matches 1415; Conservative
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TYPE: DNA
ORGANISM: Porcine circovirus
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PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/
PRIOR FILING DATE: BARLIER FILING DATE: 1998-05-21
PRIOR PLING DATE: EARLIER FILING DATE: 1998-01-22
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PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-22
PRIOR PLICATION NUMBER: EARLIER APPLICATION NUMBER: FR
PRIOR PLING DATE: EARLIER FILING DATE: 1998-03-20
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 6
SEQ ID NOS: 6
SEQ ID NO 1
LENGTH: 1767
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Pred. No. 0;
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                                                                                                                                           TYPE: DNA ORGANISM: Porcine circovirus
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Sequence 1, Application US/09583350

Requence 1, Application US/09583350

Redent No. 6517843

GRNERAL INFORMATION:

APPLICANT: Ellis, et al.

TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION A.

TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2

FILE REFERENCE: 454313-2340.1

CURRENT APPLICATION NUMBER: US/09/583,350

CURRENT FILING DATE: 1999-08-31

REGORDED OF SEQ ID NOS: 8

SOFTWARE: PALENTI VERSION 3.0

SEQ ID NO 1

LENGTH: 1767
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	RESULT 10 Sequence 1, Application US/09884514 Septiment HANDS Decrea Applicant HANDS Decrea Applicant HANDS Fearch Medellly Applicant HANDS Fearch Medellly TITLE GENERALS Fearch Medellly TITLE GENERALS ALIAN ESSENTS TITLE MEDICATION WERSEN US/09/884,514 MATCHE FILED MEDICATION WERSEN US/09/884,514 SETOR FILED MEDICATION WERSEN US/09/884,514 MATCH FILED MEDICATION WERSEN US/09/884,514 SETOR FILED DATE: 1999-10-03 SETOR MEDICATION WERSEN US/09/884,514 MATCH FILED MEDICATION WERSEN US/09/884,514 SETOR FILED MEDICATION WERSEN US/09/884,514 MATCH FILED MEDICATION WERSEN US/09/884,514 SETOR FILED MEDICATION WERSEN US/09/884,514 MATCH FILED MEDICATION WERE US/09/884,514 MATCH FILED MEDICATION WERSEN US/09/884,514 MATCH FILED ME
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| Patent No. 6217883
| GENERAL INFORMATION:
| APPLICANT: ALLAN, Gordon M.
| APPLICANT: ELLIS, John A.
| APPLICANT: KRAKOWKA, George S.
| APPLICANT: KRAKOWKA, George S.
| APPLICANT: RANCOMNET, Jean-Christophe F.
| TITLE OF INVENTION: PORCINE CIRCOVIRUS AND PARIST IN APPLICANTION WINDER: US/09/347,594
| CURRENT FILING DATE: 1999-07-01
| EARLIER APPLICATION NUMBER: 98 08777
| BARLIER FILING DATE: 1998-07-06
| WUMBER OF SEG ID NOS: 5
| SOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2.
| LEARLIER PATENTIAL NOS: 5
| SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                            79.8%; Score 1410.4;
99.6%; Pred. No. 0;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Porcine circovirus
US-09-347-594-2
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   PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
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TITLE OF INVENTION: NEW PORCINE CIRCUVIRUSES,
TITLE OF INVENTION: REAGENTS
FILE REPERENCE: ALLIAN
CURRENT PEDELICATION NUMBER: US/09/082,558A
CURRENT FILING DATE: 1998-05-21
BARLIER APPLICATION NUMBER: FR 9803707
BARLIER FILING DATE: 1998-01-22
BARLIER FILING DATE: 1998-01-22
BARLIER FILING DATE: 1998-01-23
BARLIER FILING DATE: 1998-03-30
BARLIER FILING DATE: 1998-03-30
BARLIER FILING DATE: 1998-03-30
BARLIER FILING DATE: 1998-03-30
BARLIER PAPLICATION NUMBER: FR 97/12382
BARLIER PILING DATE: 1997-10-03
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN VEY: 2.0
SOFTWARE: PALENTIN VEY: 2.0
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Best Local Similarity 99.6%;
Matches 1414; Conservative
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CRGANISM: Porcine circovirus
US-09-082-558-2
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Patent No. 6366601
GENERAL INFORMATION:
APPLICANT: ALLAN, Gordon
APPLICANT: CLARK, Edward
APPLICANT: HAINES, Deborah
APPLICANT: HANBEN, Coxi
APPLICANT: HANBEN, Coxi
APPLICANT: HARSING, John
APPLICANT: CHARREYRE, Catherine E.
APPLICANT: CHARREYRE, Catherine E.
APPLICANT: CHARREYRE, Catherine E.
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Best Local Similarity 99.6
Matches 1414; Conservative
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NUMBER OF SEQ ID NOS:
SOFTWARE: Patentin Ver
SEQ ID NO 2
LENGTH: 1767
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APPLICANT: ALLAN, Gordon
APPLICANT: ALLAN, Gordon
APPLICANT: CLARK, Edward
APPLICANT: HARINES, Deborah
APPLICANT: HARINES, Deborah
APPLICANT: HARSARD, LOTI
APPLICANT: HARBYER, Catherine E.
APPLICANT: CHARREYER, Catherine E.
APPLICANT: CHAPPUIS, Gilles E.
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION: NEW PORCINE CIRCOVIRUSES, VACCINES AND DIAGNOSTIC
TITLE OF INVENTION NUMBER: US/09/161,092
CURRENT FILING DATE: 1998-09-25
PRIOR FILING DATE: EARLIER FILING DATE: 1998-05-21
PRIOR FILING DATE: BARLIER FILING DATE: 1998-01-22
PRIOR FILING DATE: BARLIER FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: FR 9803707
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: EARLIER PILING DATE: 1998-03-20
PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-03
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Patent No. 6391314
GENERAL INFORMATION:
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	BATGGAAGTGTGGAAGCTCCTAGAACCTCAGGACAACAACGACGAGCAGCAGCAGCAGCAGCAGCAGC	948 661 1008 721 1068	1128 841 1188 901 1248	0y 1021 TITTATTATTATTATTATTONED GOOGGETTAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAATITAAAATITAAAATITAAAATITAAAATITAAAATITAAAATITAAAATITAAAATITAAAAATITAAAATITAAAAATITAAAAATITAAAAATITAAAATITAAAAATITAAAAATITAAAATITAAAATITAAAAATITAAAAATITAAAATITAAAAAA
Db 1248 GGAAGAATGCTACAGAACATCCACGAGGAGGGGCCAGTTCGTCACCCTTTCCCCCC 1307 Qy 961 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT 1020 [1141 1488 1201 1501 1548 1608	Db 1668 ATAGGCTGTGGCTTTTACAAGTTATCATCTAGAATAACGCACTGGAGCC 1727 Qy 1381 CACTCCCTGTCACCCTGGGTGATCGGGGGCCAG 1420 Db 1728 CACTCCCCTGTCACCTGGGTGATCGGGGAGCAGGGCCAG 1767 RESULT 14 US-09-583-350-2 Sequence 2, Application US/09583350 Parent No. 5617841 CONTROL 1 ANDOMATON.	APPLICANT: Ellis, et al. TITLE OF INVENTION: PREVENTION OF MYOCARDITIS, ABORTION AND INTRAUTERINE INFECTION AS TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2 TITLE OF INVENTION: WITH PORCINE CIRCOVIRUS-2 TITLE APPLICATION NUMBER: US/09/583,350 CURRENT APPLICATION NUMBER: 05/09/531 CURRENT PILING DATE: 1999-08-31 NUMBER OF SEQ ID NOS: 8 SOFTWARE: PARCHING DATE: 1999-08-31 SOFTWARE: PARCHING DATE: 1999-08-31 TUMBER OF SEQ ID NOS: 8 SOFTWARE: PARCHING DATE: 1999-08-31 TUMBER OF SEQ ID NOS: 8 SOFTWARE: PARCHING DATE: 1999-08-31 TYPE: DNA TYPE: DNA TYPE: DNA	Ouery Match Query Match Query Match Best Local Similarity 9.6%; Pred. No. 0; Red. Calcal Similarity 9.6%; Pred. No. 0; Best Local Similarity 9.6%; Pred. No. 0; Red. Calcal Similarity 9.6%; Pre

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               CTGCTAATTTTGCAGACCCGGAAACCACATACTGGAAACCACCTAGAAACAAGTGGTGGG
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| GENERAL INFORMATION:
| APPLICANT: ALLAN, Gordon
| APPLICANT: ALLAN, Gordon
| APPLICANT: ALLAN, Brian
| APPLICANT: HANSARD, Lori
| APPLICANT: HANSARD, Lori
| APPLICANT: HARREYER, Catherine E.
| APPLICANT: CHARREYER, Fancis McNeilly
| TITLE OF INVENTION: NEW PORCINE CIRCOVINUSES, VACCINES AND DIAGNOSTIC
| TITLE OF INVENTION: NEW PORCINE CIRCOVINUSES, CURRENT APPLICATION NUMBER: FR 9800873
| FILING DATE: 1998-01-22
| PRIOR FILING DATE: 1998-01-22
| PRIOR FILING DATE: 1998-03-20
| PRIOR FILING DATE: 1997-03-30
| SEQ ID NO 2
| LERGTH: 1767
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Pred. No. 0;
0; Mismatches
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Patent No. 6660272
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Best Local Similarity 99.64;
Matches 1414; Conservative
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ORGANISM: Porcine circovirus
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ALIGNMENTS

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The present invention describes a new isolated porcine circovirus Type II (PCVII), obtained from postweaning multisystemic wasting syndromeaffected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences. AAX434934 represent PCVII open reading frame (ORF) proteins (N.B. the PCVII ORFS given in Fig 2A to Fig 2B do not correspond exactly with the PCVII ORFS given in Fig 3A to Fig 3D). The PCVII polypeptides can be used for treating or preventing PCVII infection in vertebrates. The products can also be used to detect the PCVII
                                                                                                                     Porcine circovirus type II; PCVII; PCVI; pig; infection; vaccine; postweaning multisystemic wasting syndrome virus; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1768 BP; 454 A; 361 C; 492 G; 461 T; 0 U; 0 Other;
                                                                                        Porcine circovirus type II 412 nucleotide sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated porcine circovirus Type II.
AAX83754 standard; DNA; 1768 BP.
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                                                           27-AUG-1999 (first entry)
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AAZ56871 AAF75837 AAF75838 us-10-718-264-15.rng

1021 TITELTEATICALTICALTIAGGGTTCAACTGGGGGGTTCTTAAAATTCTCTGAATTGT 1030	RESULT 2 AAF75841 standard; DNA; 1768 BP. XX AAF75841; XX XX AAF75841; XX DF 06-AUG-2003 (revised) DT 18-MAY-2001 (first entry) XX XX DE PCV DNA fragment of Imp 1121 strain. XX
Queery Match 93.11\$, Score 1645.6; DB 2; Length 1768; Desert Local Similarity 96.01; Press No. Matches 1699; Conservative 0; Missierches 69; Indels 1; Gaps 1; ACCAGOGCACTICOGCACCACCACCACCACACACACACACACACACACACAC	OY 721 ATGATCTACTGAGACTGTGATCGATACCATTGACTGAGGACTGAAGGTGGAACTG 780

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Krakowka
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                                                                         AAAACGAAAGAAGTGCGCTGTAAGTATT 1767
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CE, Chappuis GE,
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31-MAY-2000; 2000US-00583350.
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(UYSA-) UNIV SASKATCHEWAN.
(UYBE-) UNIV QUEENS BELFAST.
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(first entry)
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Best Local Similarity 95.6
Matches 1691; Conservative
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                                                                                           GCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTTTTCCTTC
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                                                                                     CCACTCCCCTGTCACCCTGGGTGATCGGGGGGGGGGCCAGAATTCAACCTTAACCTTTC
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                                                                                                                                                                                                                                                                                                                                                              mammalian circovirus; virus culture; gene; ss
                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of porcine circovirus 2 (PCV2)
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/*tag= a
/note= "ORF1; encodes ABB99414"
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The present sequence represents the complete genome of porcine circovirus 2 (PCV2). This sequence comprises two open reading frames (ORFs). PCV2 is cultured using the method of the invention. The specification describes a method for culturing a mammalian circovirus. The method comprises obtaining mammalian cells are permissive for mammalian dircovirus El function, where the cells are permissive for mammalian dircovirus El function, introducing the mammalian circovirus genome, or its portion, into the mammalian cells, and culturing the mammalian cells under conditions suitable for replication of the mammalian circovirus. The method of the invention is useful for culturing circovirus in mammalian cells, expressing mammalian adenovirus El function for molecular biology, and biotechnology purposes. (Updated on 27-0CT-2003 to standardise OS field)
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                                                                                                                                               Culturing a mammalian circovirus in mammalian cells expressing mammalian adenovirus El function, useful for molecular biology and biotechnology
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95.1%; Pred. No. 0;
ive 0; Mismatches
                                         Babiuk LA;
                                                                                                                                                                                                                                             Disclosure; Fig 3A; 23pp; English
                                         Willson P,
                                                                                WPI; 2003-029933/02.
P-PSDB; ABB99414, ABB99415.
(UYSA-) UNIV SASKATCHEWAN
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Matches 1682; Conservative
                                         Tikoo SK,
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TIGIGAAGAAGCAGACTITIAATAAAGIGAAGIGGIATITIGGGIGCCCGCIGCCACAICG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a new isolated porcine circovirus Type II (PCVII), obtained from postweaning multisystemic wasting syndrome-affected pigs. AAX83754 to AAX83757 represent PCVII nucleotide sequences. AAX2429 to AAX44934 represent PCVII open reading frame (ORF) proteins with the PCVII ORFs given in Fig 2A to Fig 2B do not correspond exactly with the PCVII ORFs given in Fig 3A to Fig 3D). The PCVII polypeptides can be used for treating or preventing PCVII infection in vertebrates. The products can also be used to detect the PCVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1681 GAIGGCIGCGGGGGCGGIGICIICTICIGCGGIAACGCCITCGAIACGICAIAGCIG 1740
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                                                                                                                                                                                                       circovirus type II; PCVII; PCVI; pig; infection; vaccine;
ning multisystemic wasting syndrome virus; diagnosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1786;
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                                                                                                                                                                                   Porcine circovirus type II 9741 nucleotide sequence
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Pred. No. 0;
0; Mismatches 86;
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                            AAAACGAAAGAAGTGCGCTGTAAGTATT
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Best Local Similarity 94.3%;
Matches 1673; Conservative (
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16-DEC-1997;
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        CTGCTAATTTTGCAAACCCGGGAAACCACATACTGGAAACCACCTAAAAACAAGTGGTGGG
                                                                                            ATGATCTACTGAGACTGTGTGATCGATATCCATTGACTGTAGAGACTAAAAGGTGGAACTG
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                                GGAAGAAAGTCATTAATATTGAATCTCATGTCCACCGCCCAGGAGGGGGGTTCTGACT
                                                                                                                                                  GTGGTTCGCTTGACAGTATATCCGAAGGTGCGGGAGAGGCGGGTGTTGAAGATGCCATTT
                                                                                                                                                                TTCCTTCTCCAGCGGTAACGGT -----GGCGGGGGTGGACCAGCCAGCGGGGGGGGGG
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                      CTGGAGCCCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAGAATTCAACCTTA
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                                                                                                                                                                                                                                                                                   ATACGTCATATCTGAAAAC-GAAAGAAGTGCGCTG 1759
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                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of PCV isolate Imp1011-48121
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Charreyre CE, Chappuis GE;
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98FR-00000873.
98FR-00003707.
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                The present sequence represents the nucleotide sequence of PCV isolate Imp1011-48121. The specification describes a preparation of type II porcine circovirus (PCV), which is particularly isolated from a lesion, from a pig with symptoms of PMMS (porcine multisystemic wasting syndrome). PCV (attenuated or inactivated), polypeptides derived from it, and vectors that express these polypeptides are all useful in vaccines, suitable for administration to adult or young pigs, or to prepant sows (for passive immunization of their offspring). DNA isolated from PCV is used for in vivo or in vitro expression of viral polypeptides, also as probes or primers for diagnosis in usual hybridization or amplification assays. These polypeptides may also be used diagnostically to detect PCV-specific antibodies, while antibodies raised against the polypeptides can be used to detect antigens, in any usual immunoassay format
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                 1128 TACCTTTTTTGGCCCGCAGTATTCTGATTACCAGCAATCAGACCCGGTTGGAATGGTACT
                                                                                         GGAAGAATGCTACAGAACAATCCACGGAGGAAGGGGCCAGTTCGTCGTCACCTTTCCCCCC
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                     1128 TACCTITITIGGCCCCCCAGTATTCTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT
                                               CCTCAACTGCTGTCCCAGCTGTAGAAGCTCTTTATCGGAGGATTACTTCCTTGGTATTTT
                                                            1308 CATGCCCTGAATTTCCATATGAAATAAATTACTGAGTCTTTTTTATCACTTCGTAATGGT
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                                             antigen for
                                                                                               The invention provides a novel antigenic preparation directed against porcine multisystemic wasting syndrome (PMWS) that comprises porcine circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV antigens and PPV antigens can be used for vaccination against PMWS. The present sequence represents the DNA sequence of PCV IMp.1011-48121
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                                           Use of a porcine circovirus antigen and a porcine parvovirus vaccination against porcine multisystemic wasting syndrome.
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porcine multisystemic
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                                                                                                                                                                                     The present invention relates to the use of porcine circovirus-2 (PCV-2) immunogen to formulate a vaccine composition to prevent or treat pigs against myocarditis and/or abortion and/or intrauterine infection and/or post-weaning, multisystemic wasting syndrome and other pathological sequalse associated with PCV-2. The present sequence is a DNA fragment of a strain of PCV, which was used in the present invention. (Updated on 06-AUG-2003 to correct OS field.)
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                                                                                         Use of porcine circovirus-2 immunogen to formulate a vaccine composition to treat pigs against myocarditis, abortion, intrauterine infection and/or post-weaning, multisystemic wasting syndrome associated with PCV-2.
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                            Hassard L;
Audonnet J
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                                                                                                                                                                                                                                                                                           Sequence 1767 BP; 447 A; 360 C; 502 G; 458 T; 0 U; 0 Other;
                             gs,
                            , Haines |
Krakowka (
                             E)
                            Meehan B, Clark E
CE, Chappuis GE,
                                                                                                                                                                   Disclosure, Fig 1 #2; 134pp; English
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Best Local Similarity 99.6%;
Matches 1415; Conservative
      (UYBE-) UNIV QUEENS BELFAST
                            Ellis JA, Allan GM, Harding J, Charreyre Mcneilly F;
                                                                              WPI; 2001-244408/25.
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                                                               ATGATCTACTGAGACTGTGATCGATATCCATTGACTGTAGAGACTAAAAGGTGGAACTG
                                                                                                                                                           TACCITITITIGGCCCGCAGTATICTGATTACCAGCAATCAGACCCCGTTGGAATGGTACT
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                                                                                                     Hassard
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;
                                                                                                       Haines D,
                                                                                                    E, Ellis J,
Chappuis GE;
                                                                                                                                                                    New type II porcine circovirus
      97FR-00012382.
98FR-00000873.
98FR-00003707.
                                                                                                                                                                                            Claim 11; Fig 2; 56pp; French
                                                       (MERI-) MERIAL.
(UYBE-) UNIV QUEENS BELFAST.
(UYSA-) UNIV SASKATCHEWAN.
                                                                                                       Clark
                                                                                                                   Charreyre CE,
                                                                                                        Meehan B,
                                                                                                                                            WPI; 1999-264024/22
      03-OCT-1997;
22-JAN-1998;
20-MAR-1998;
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                                                                                                                                                                                                                                                                                                                                                         New type II porcine circovirus, used for, e.g. passive immunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1410.4; DB 2; Length 1767;
Pred. No. 0;
0; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                            Hassard L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1767 BP; 448 A; 359 C; 500 G; 460 T; 0 U; 0 Other;
   wasting syndrome; pig; vaccine; ss
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Chappuis GE;
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Best Local Similarity 99.6'
Matches 1414; Conservative
porcine multisystemic
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                                        Porcine circovirus
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Harding J,
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GTACCTTGTTGGAGAGCGGGAGTCTGGTGACCGTTGCAGAGCAGCACCTGTAACGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                 The invention provides a novel antigenic preparation directed against porcine multisystemic wasting syndrome (PWMS) that comprises porcine circovirus (PCV) antigen and porcine parvovirus (PPV) antigen. The PCV antigens and PPV antigens can be used for vaccination against PMMS. The present sequence represents the DNA sequence of PCV Imp.1011-48285.
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                                                                        porcine multisystemic wasting syndrome; PMWS; antiviral;
circovirus; PCV; porcine parvovirus; PPV; vaccination; ds
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Pred. No. 0;
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                                               Imp.1011-48285 isolate
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multisystemic
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Best Local Similarity 99.6%;
Matches 1414; Conservative
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UNIV SASKATCHEWAN.
                          entry
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                                                DNA sequence of PCV
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porcine circovirus;
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                                                                                                                Porcine circovirus
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Audonnet J
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Pred. No. 0;
0; Mismatches 6; Indels 0;
                                                                                                  Vaccine; pig; myocarditis; abortion; intrauterine infection;
multisystemic wasting syndrome; ds.
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Krakowka GS,
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                                                                     PCV DNA fragment of Imp 1011-48285 strain.
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uis GE,
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CE, Ch
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(UYSA-) UNIV SASKATCHEWAN.
(UYBE-) UNIV QUEENS BELFAST.
                       (revised)
(first entry)
                                                                                                                                                Porcine circovirus type 2.
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Harding J, (
Mcneilly F;
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                                                                                                                                                                                                                                                      PCV isolate; type II porcine circovirus; PCV; PMWS; porcine multisystemic wasting syndrome; pig; vaccine; ss.
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                                                                                                                                                                                                                  Nucleotide sequence of PCV isolate Imp1010.
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Chappuis GE;
                                                                                             AAX35381 standard; DNA; 1768 BP.
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(UYBE-) UNIV QUEENS BELFAST.
(UYSA-) UNIV SASKATCHEWAN.
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Harding J, Charreyre CE,
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Best Local Similarity 96.7
Matches 1374; Conservative
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1368 TITIATIATICATITAGGGTTTAAGTGGGGGGTCTTTAAGATTAAATTCTGTAATTGTA
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75.6%; Score 1335.4; DB 2; Length 1768;
Best Local Similarity 96.7%; Pred. No. 0;
Matches 1374; Conservative 0; Mismatches 46; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hassard L;
                                                                                                                                                                                                                                                                                       Nucleotide sequence of PCV isolate Imp999 (corrected version)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1768 BP; 453 A; 360 C; 494 G; 461 T; 0 U; 0 Other;
                                                                                             1420
                                                                                                           wasting syndrome; pig; vaccine;
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                                                                                                                                                                                                                                                                                                                      porcine circovirus; PCV; PMWS;
                                                                                             CCACTCCCCTGTCACCCTGGGTGATCGGGGAGCAGGGCCAG
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Charreyre CE, Chappuis GE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New type II porcine circovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97FR-00012382.
98FR-00000873.
98FR-00003707.
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                                                                                                                                                                                                 AAX35380 standard; DNA; 1768
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UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                    PCV isolate; type II p
porcine multisystemic
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22-JAN-1998;
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